

Report

	assembly
# contigs (>= 1000 bp)	8
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	2
Total length (>= 1000 bp)	6765070
Total length (>= 5000 bp)	6749582
Total length (>= 10000 bp)	6749582
Total length (>= 25000 bp)	6749582
Total length (>= 50000 bp)	6749582
# contigs	12
Largest contig	4031312
Total length	6767661
Reference length	2730326
GC (%)	39.45
Reference GC (%)	32.85
N50	4031312
NG50	4031312
N75	2718270
NG75	4031312
L50	1
LG50	1
L75	2
LG75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	0 + 1 part
Unaligned length	4025258
Genome fraction (%)	99.988
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.96
# indels per 100 kbp	17.58
Largest alignment	2718270
Total aligned length	2742373
NGA50	2718270
NGA75	2718270
LGA50	1
LGA75	1

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

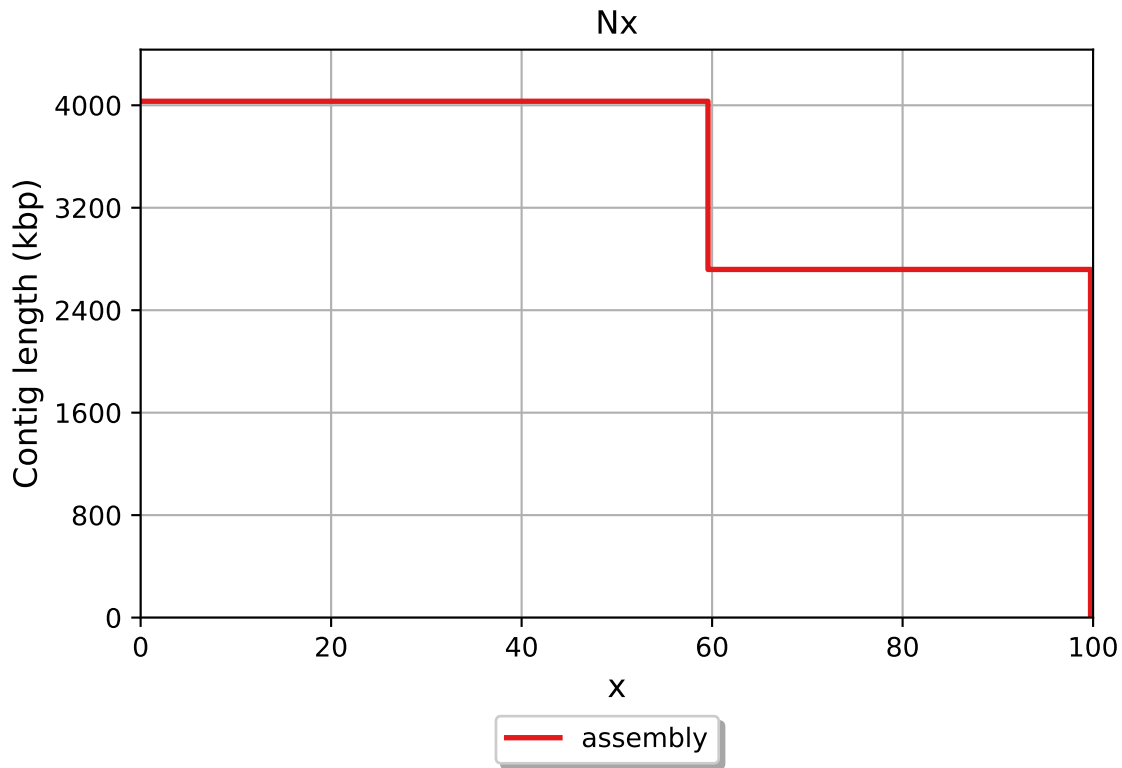
	assembly
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	108
# indels	480
# indels (<= 5 bp)	478
# indels (> 5 bp)	2
Indels length	594

All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

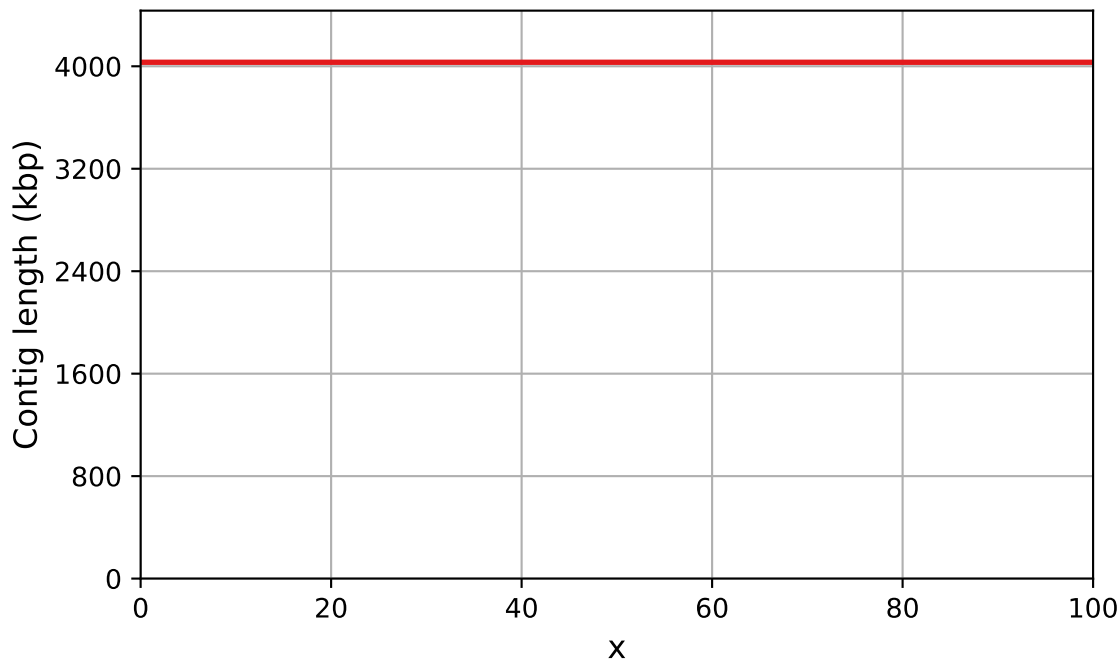
Unaligned report

	assembly
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	4025258
# N's	0

All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

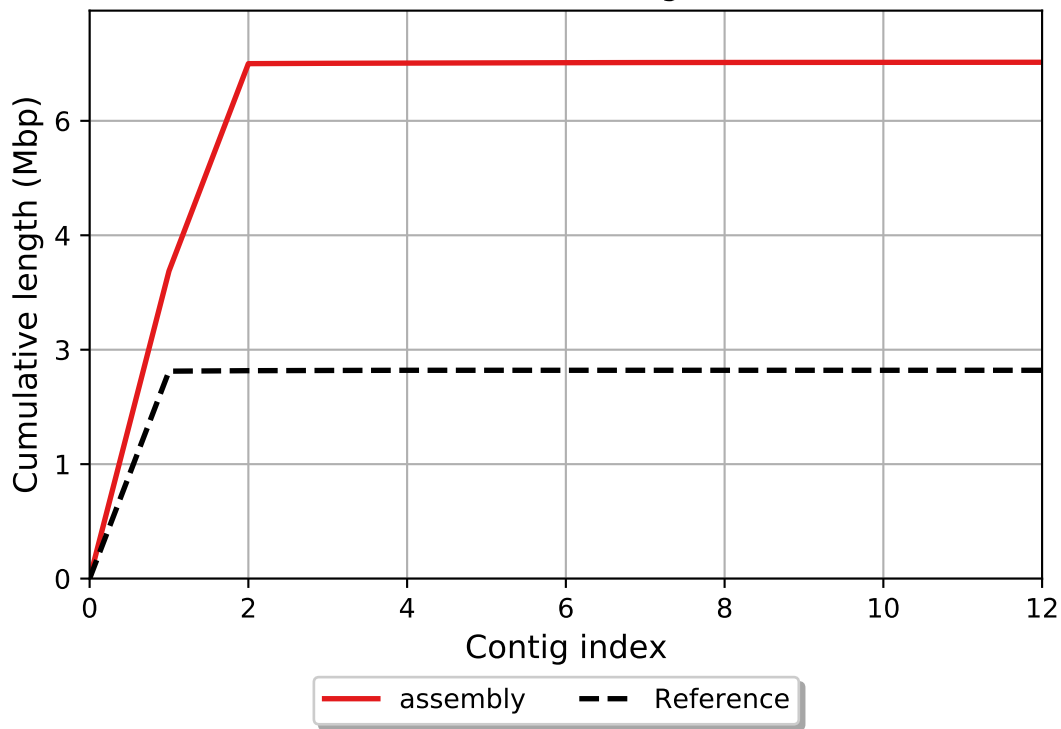


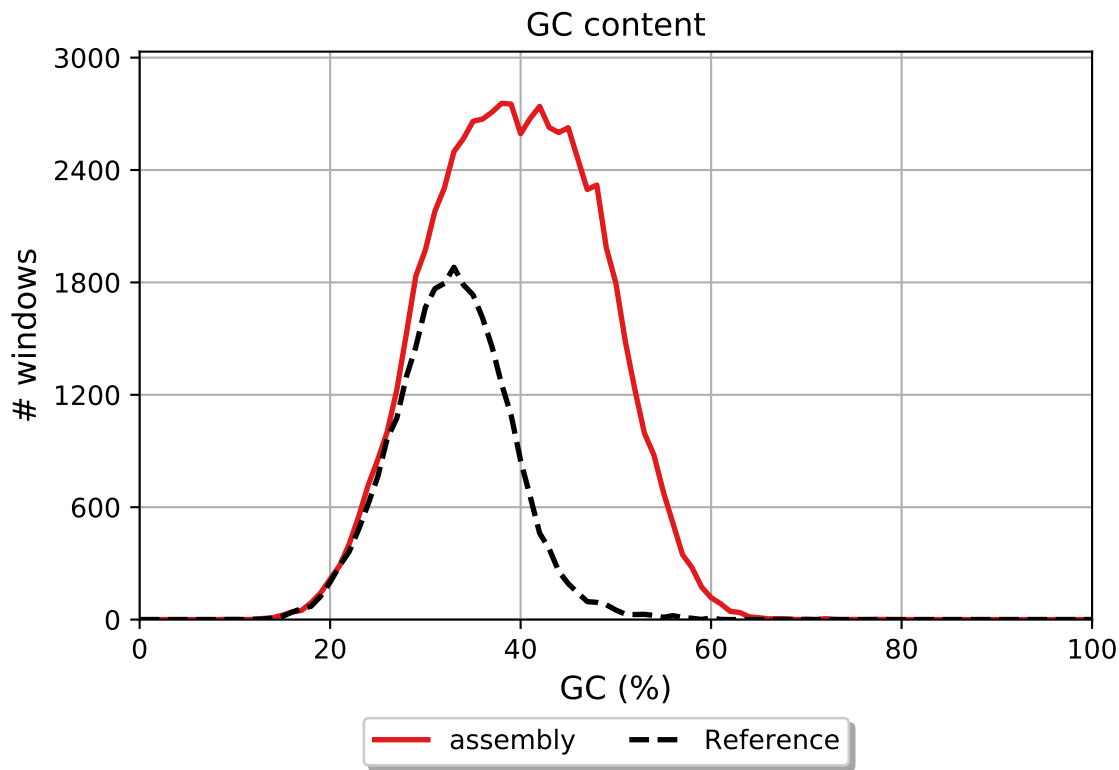
NGx



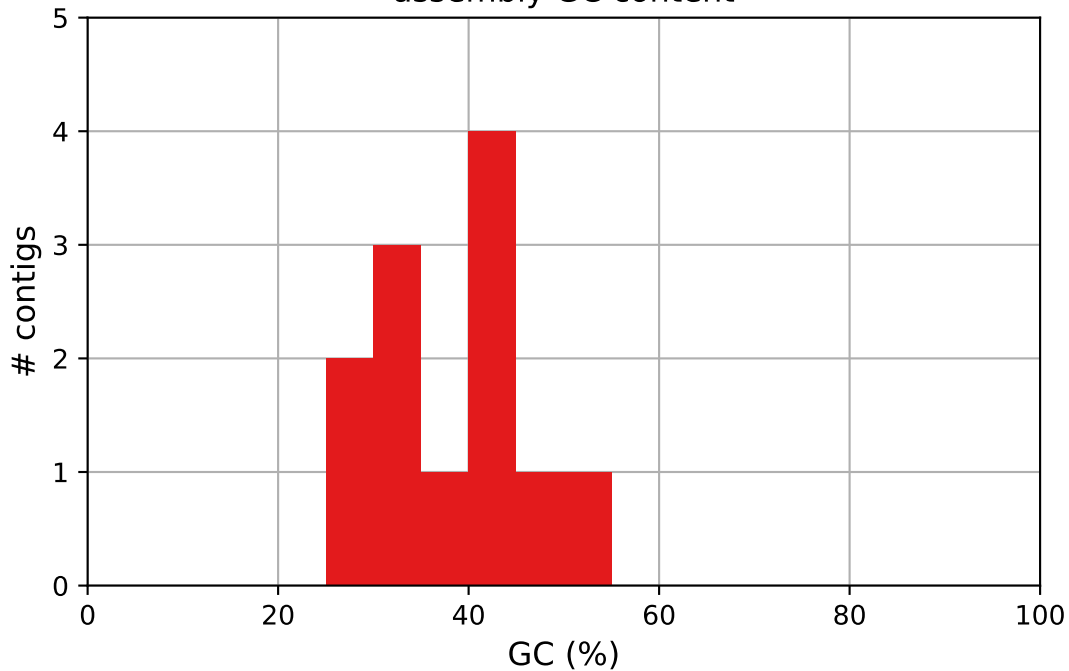
— assembly

Cumulative length



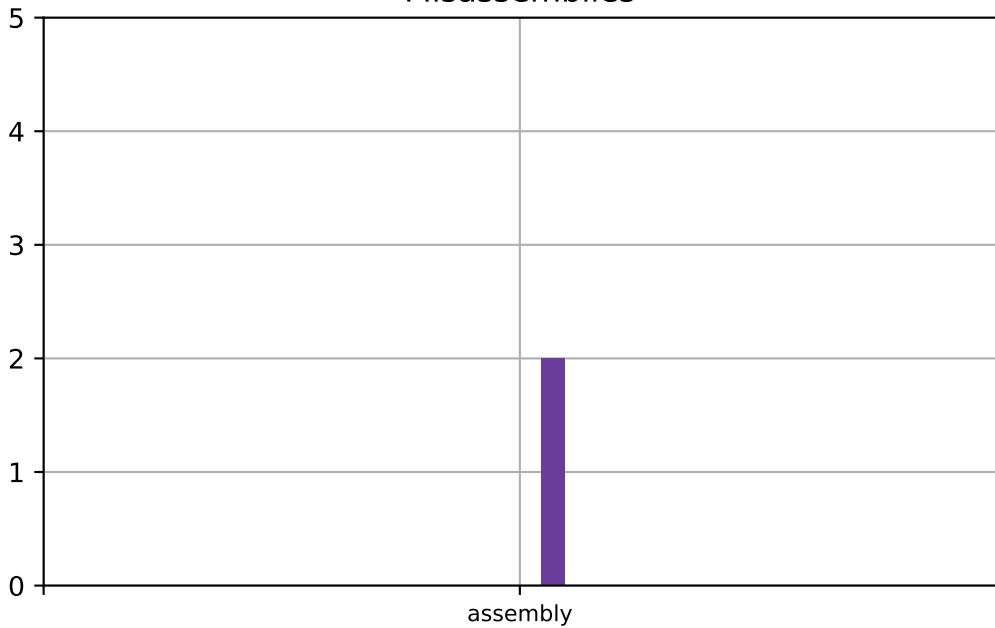


assembly GC content



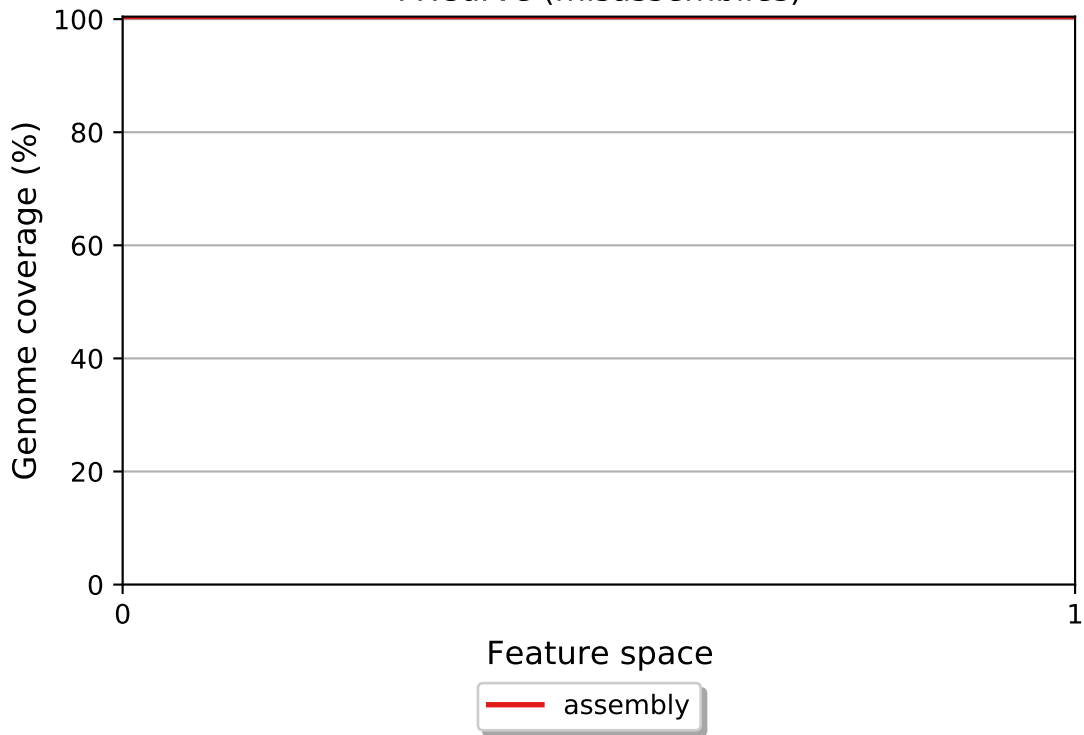
assembly

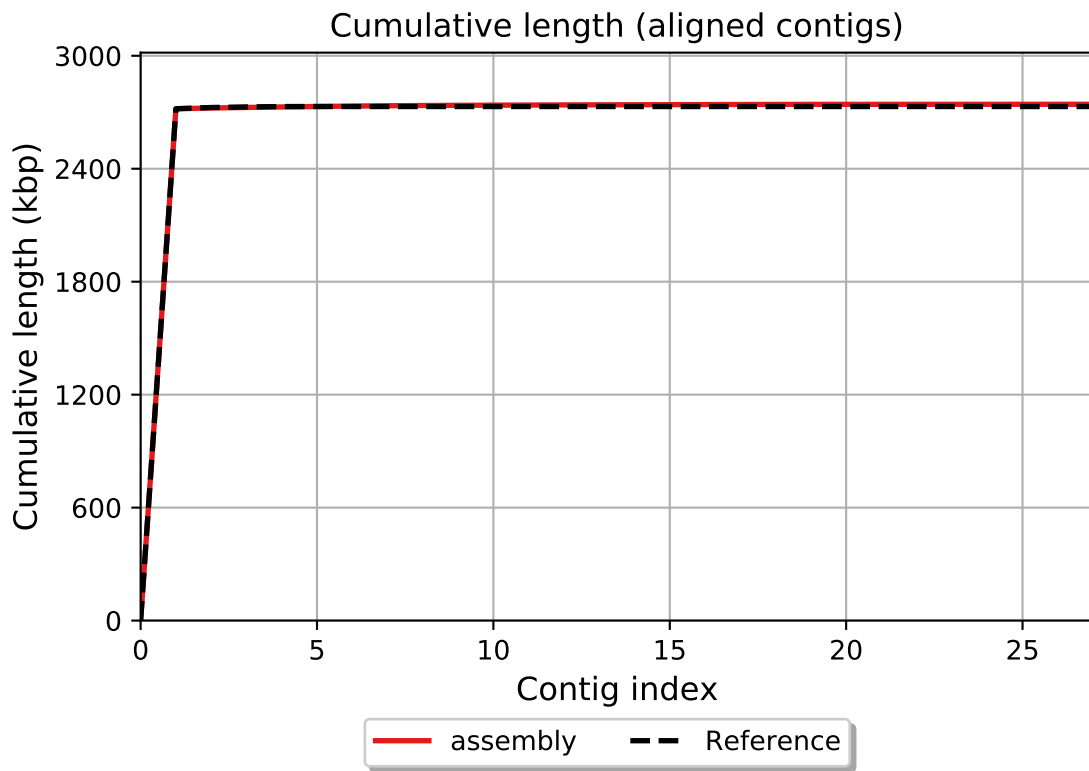
Misassemblies



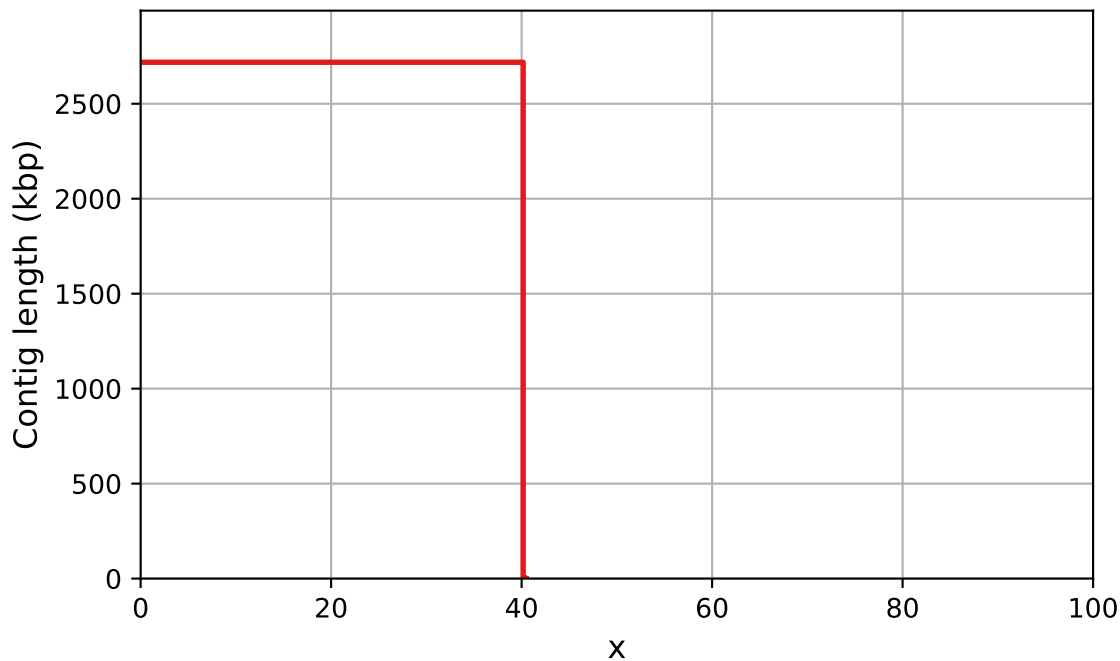
interspecies translocations

FRCurve (misassemblies)



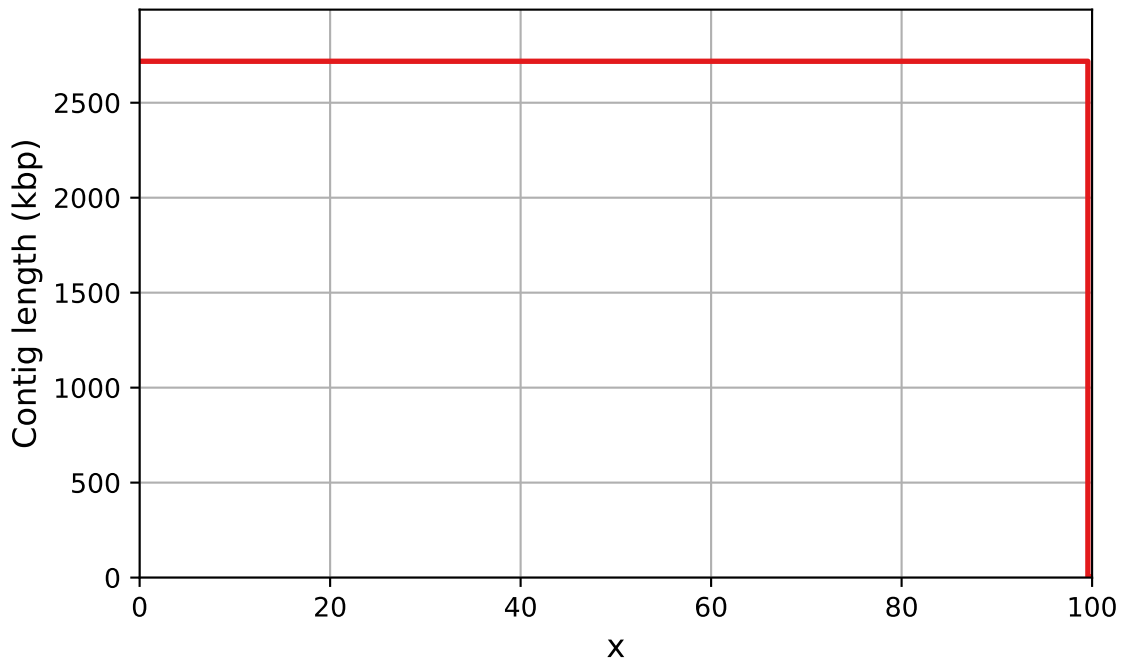


NAx



— assembly

NGAx



— assembly